

Supplementary Information – S1 Text

Sexual selection in females and the evolution of polyandry

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Figures A - E

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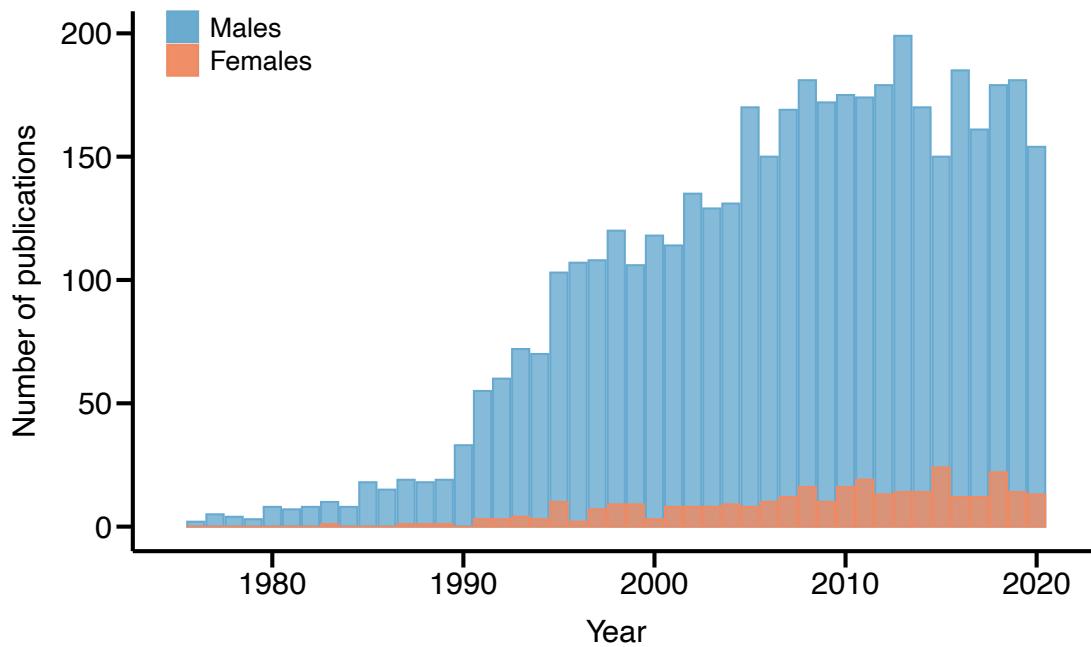


Figure A. Imbalance between studies of sexual selection in males and females. Bars indicate a strong male bias in the number of published articles on sexual selection indexed in ISI Web of Science (Clarivate Analytics) between 1900-2021. Data obtained from topic search using the search terms “sexual selection AND (male choice OR female competition)” for female and “sexual selection AND female choice OR male competition” for male search. This is not meant to provide an exhaustive search of publications on sexual selection but to showcase the publication bias towards male studies focusing on Darwinian sexual selection in terms of competition for and choice of mating partners.

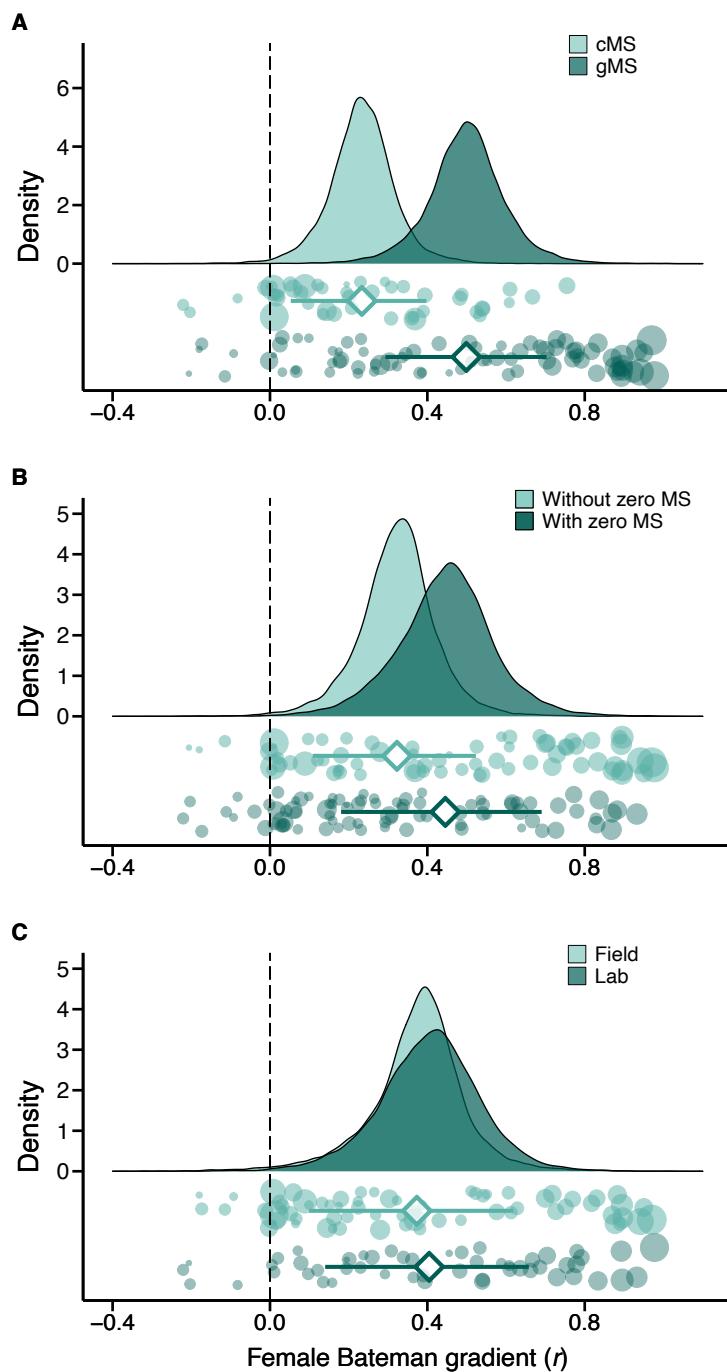


Figure B. Methodological predictors of female Bateman gradients. Raincloud charts showing effects of mating success method (*cMS*: copulatory mating success, *gMS*: genetic mating success), mating success range (with or without zero mating success (MS) category) and study type (field versus laboratory studies) on female Bateman gradients (see also Table 2 and Table C in S1 Text). The code and data needed to generate this figure can be found at https://salomefromonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

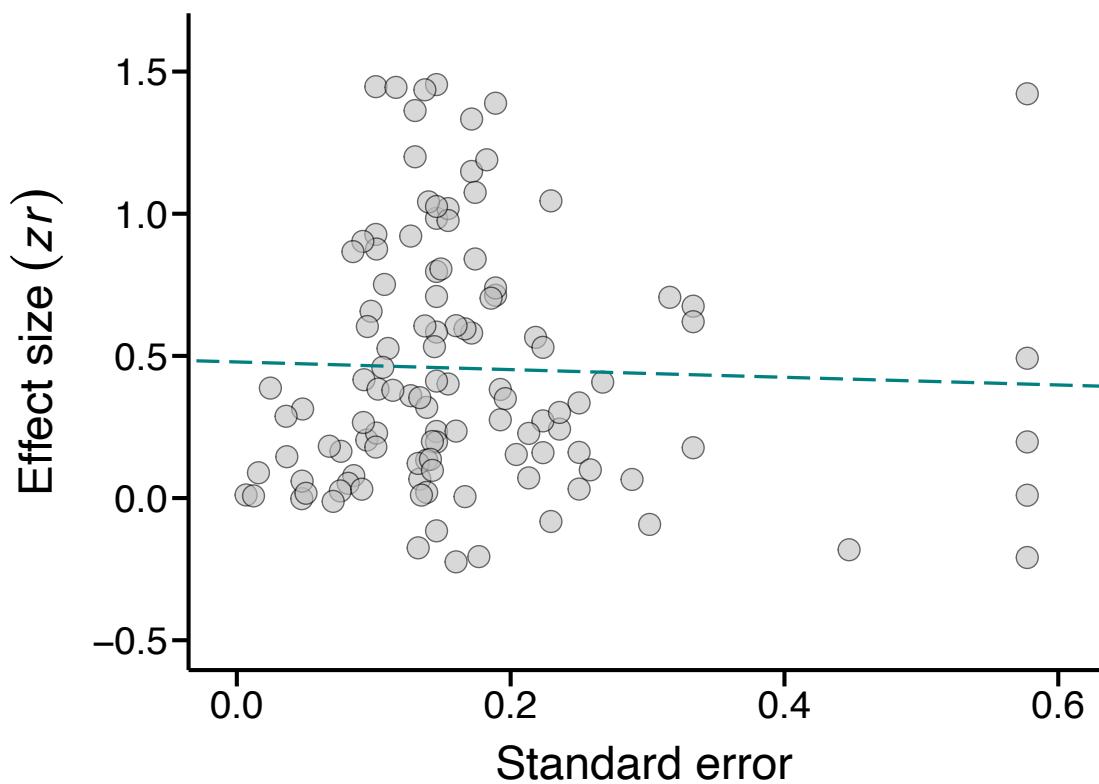


Figure C. Egger's regression. Relationship between effect size Fisher's z and its standard error testing whether small studies (i.e., those with smaller sample sizes and lower precision) are more likely to be published when reporting larger effect sizes. Dashed line shows the regression fit. The code and data needed to generate this figure can be found at https://salomefrommonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

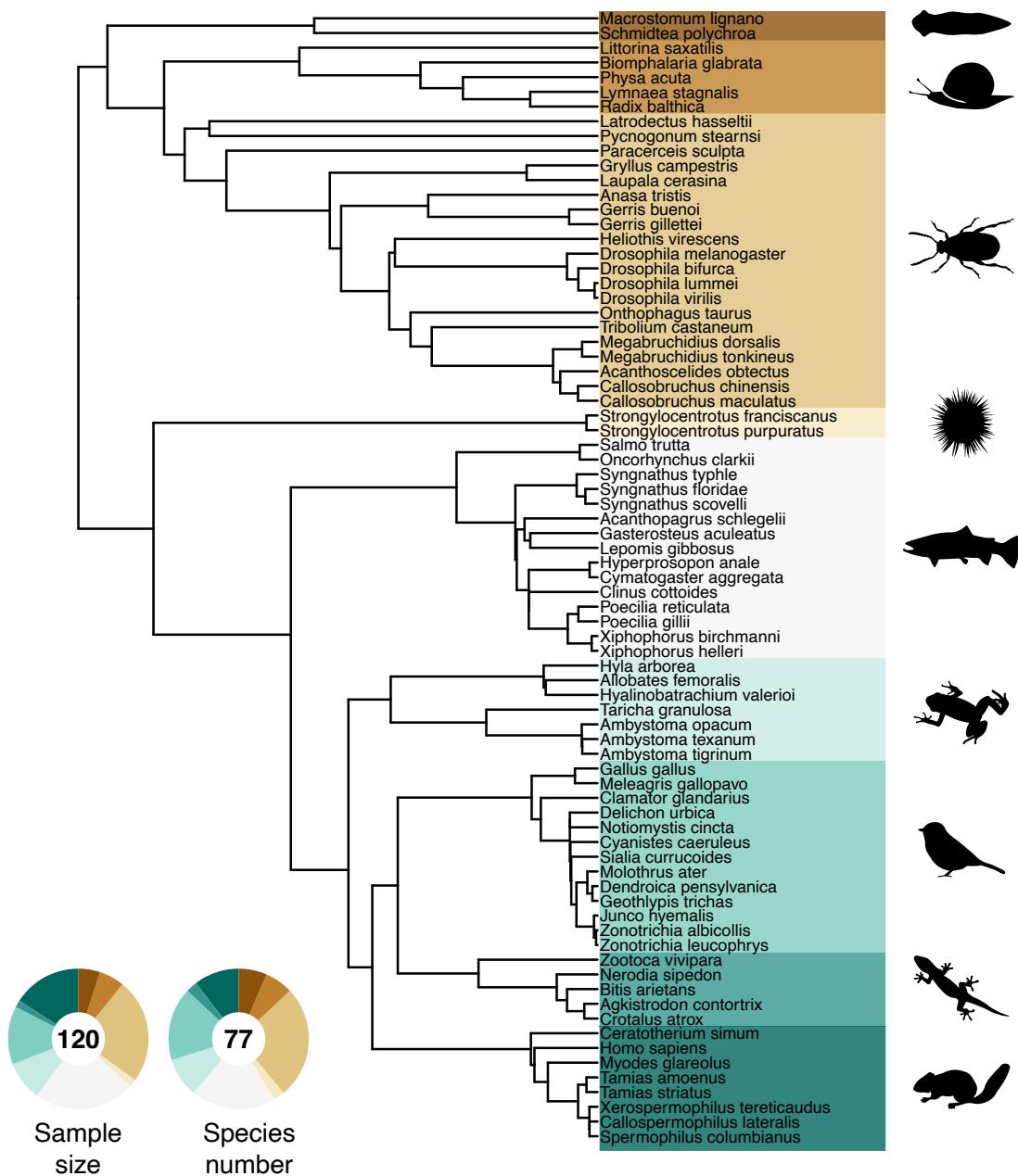


Figure D. Phylogenetic tree of all sampled species. Doughnut charts show the relative fraction of the sampled effect sizes (i.e., number of Bateman gradients) and the number of species.

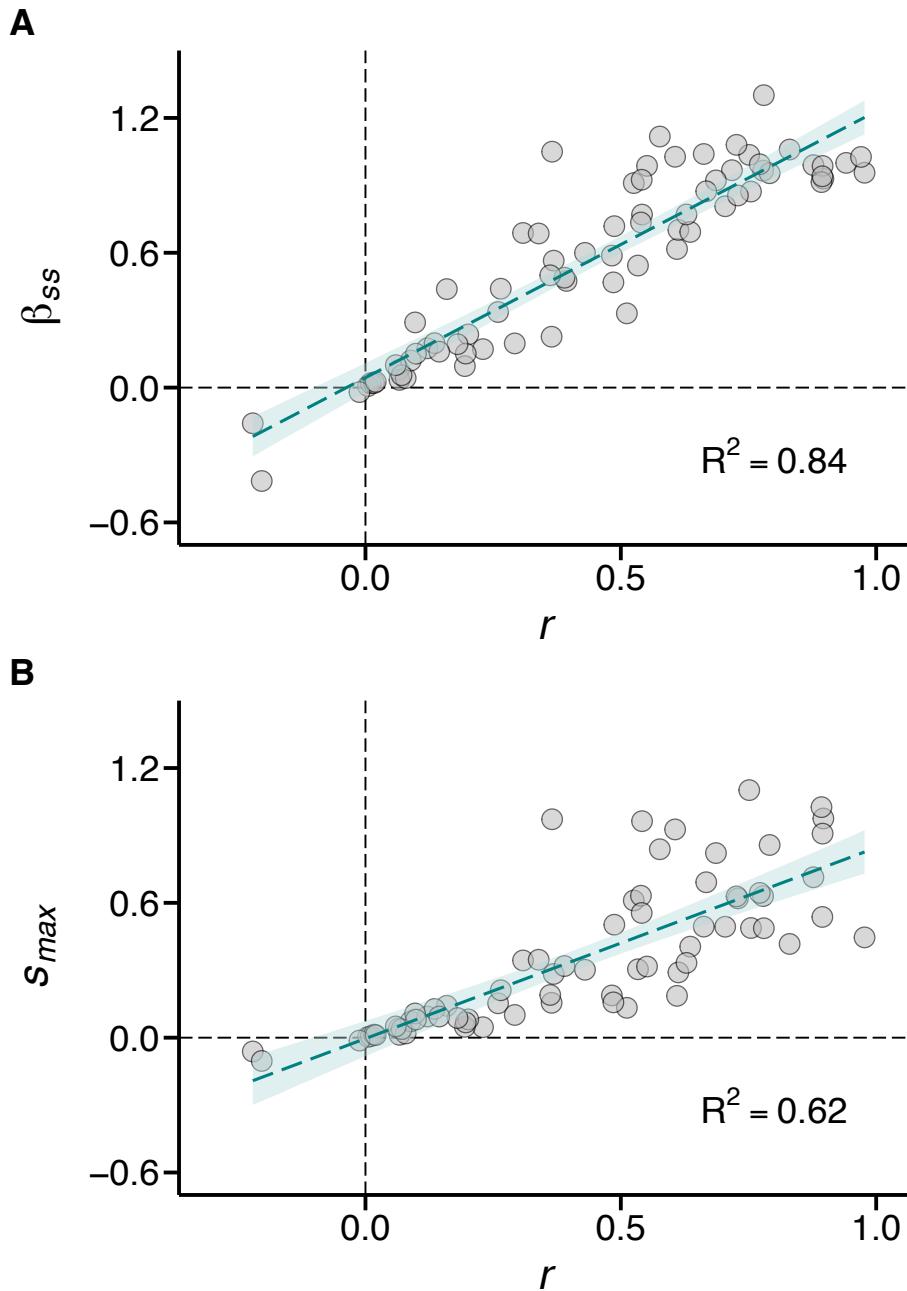


Figure E. Significance of used effect size. Relationship between effect size r (correlation coefficient) and (A) the actual Bateman gradient (β_{ss}) and (B) the maximum standardized sexual selection differential (s'_{max}). Graphs show a subset of data for which (A) standardized Bateman gradients were available ($N = 74$) and (B) estimates of the variance in relativized mating success could be extracted from primary studies ($N = 73$). Dashed line shows the linear regression fit with shaded area indicating the 95% confidence intervals. The code and data needed to generate this figure can be found at https://salomefrommonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

Table A. Global tests of sexual selection in females using the restricted maximum likelihood (REML) approach. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the entire dataset (global model) and subsets with respect to mating success method (copulatory versus genetic), mating success range (including versus excluding zero mating success category), study type (laboratory versus field studies) and mating system (low-polyandry versus high-polyandry species). Table shows number of effect sizes (k), number of species (N) and estimates of r together with 95% confidence intervals (in parentheses).

Model	k	N_{Species}	Global effect size			P -value
			r	(95% CI)	z -value	
Global model	120	77	0.37	(0.15, 0.59)	3.33	0.001
Copulatory mating success	43	24	0.23	(0.06, 0.41)	2.66	0.008
Genetic mating success	79	56	0.50	(0.32, 0.68)	5.41	< 0.001
Including zero mating success	70	42	0.43	(0.18, 0.68)	3.34	0.001
Excluding zero mating success	79	58	0.32	(0.17, 0.48)	4.09	< 0.001
Laboratory studies	52	31	0.40	(0.15, 0.65)	3.10	0.002
Field studies	68	47	0.40	(0.31, 0.49)	8.96	< 0.001
High-polyandry species	32	16	0.23	(0.09, 0.37)	3.16	0.002
Low-polyandry species	88	61	0.41	(0.16, 0.66)	3.20	0.001

Table B. Comparison of Bateman gradients among major taxonomic groups.

Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown all classes for which at least 10 effect sizes have been obtained from the literature. Table shows number of effect sizes (k), number of species (N), and effect sizes (r) with posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Taxonomic group	k	N_{Species}	Effect size		P_{MCMC}
			r	(Posterior mode, HPD)	
Arthropoda	29	20	0.38	(0.25, 0.52)	< 0.001
Actinopterygii	28	15	0.59	(0.45, 0.73)	< 0.001
Amphibia	11	7	0.47	(0.21, 0.72)	0.005
Aves	16	13	0.37	(0.20, 0.51)	< 0.001
Mammalia	19	8	0.37	(0.15, 0.60)	0.004

Table C. Predictors of inter-specific variation in female Bateman gradients using restricted maximum likelihood (REML) approach. Methodological moderators include mating success method (copulatory versus genetic mating success), mating success range (including versus excluding mating success category), study type (field versus lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry (continuous variable) estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Phylogenetically controlled multilevel meta-analytic single predictor models are shown with Omnibus tests (Wald-type chi-square test) and McFadden's R^2 .

Moderator	Estimate \pm SE	Q_M	P-value	R^2
Mating success method	0.28 \pm 0.09	10.71	0.001	0.23
Mating success range	0.16 \pm 0.06	6.48	0.011	0.14
Study type	0.07 \pm 0.09	0.62	0.429	0.03
Year	0.00 \pm 0.01	0.67	0.414	0.01
Mating system	0.31 \pm 0.07	16.92	< 0.001	0.35
Polyandry	0.66 \pm 0.14	23.30	< 0.001	0.47

Table D. Estimates of polyandry used to assess the mating system classification (low-polyandry and high-polyandry species). Table shows estimates of all 77 sampled species in alphabetical order together with reference.

Species	Polyandry	Reference
<i>Acanthopagrus schlegelii</i>	0.920	[1]
<i>Acanthoscelides obtectus</i>	0.551	*
<i>Agkistrodon contortrix</i>	0.520	[2]
<i>Allobates femoralis</i>	0.571	[3]
<i>Ambystoma opacum</i>	0.294	[4]
<i>Ambystoma texanum</i>	0.857	[5]
<i>Ambystoma tigrinum</i>	0.467	[6]
<i>Anasa tristis</i>	0.950	[7]
<i>Biomphalaria glabrata</i>	0.654	[8]
<i>Bitis arietans</i>	0.941	[9]
<i>Callosobruchus chinensis</i>	0.680	[10] †
<i>Callosobruchus maculatus</i>	1.000	[10] †
<i>Callospermophilus lateralis</i>	0.630	[11]
<i>Ceratotherium simum</i>	0.697	[12]
<i>Clamator glandarius</i>	0.308	[13]
<i>Clinus cottoides</i>	0.826	[14]
<i>Crotalus atrox</i>	0.400	[15]
<i>Cyanistes caeruleus</i>	0.470	[16]
<i>Cymatogaster aggregata</i>	0.800	[17]
<i>Delichon urbica</i>	0.235	[18]
<i>Dendroica pensylvanica</i>	0.606	[19]
<i>Drosophila bifurca</i>	0.326	[20] ††
<i>Drosophila lummei</i>	0.753	[21] ††
<i>Drosophila melanogaster</i>	0.759	[22]
<i>Drosophila virilis</i>	0.753	[21] ††
<i>Gallus gallus</i>	0.950	[23] †
<i>Gasterosteus aculeatus</i>	0.783	[24]
<i>Geothlypis trichas</i>	0.654	[25]
<i>Gerris buenoi</i>	1.000	[26]
<i>Gerris gillettei</i>	0.776	[27]
<i>Gryllus campestris</i>	0.809	[28]
<i>Heliothis virescens</i>	0.655	[29]
<i>Homo sapiens</i>	0.012	[30]
<i>Hyalinobatrachium valerioi</i>	0.736	[31]
<i>Hyla arborea</i>	0.158	[32]
<i>Hyperprosopon analis</i>	1.000	[17]
<i>Junco hyemalis</i>	0.439	[33]
<i>Latrodectus hasselti</i>	0.667	[34]
<i>Laupala cerasina</i>	1.000	[35]
<i>Lepomis gibbosus</i>	0.244	[36]

Species	Polyandry	Reference
<i>Littorina saxatilis</i>	0.680	[37]
<i>Lymnaea stagnalis</i>	0.588	[38]
<i>Macrostomum lignano</i>	1.000	[39]
<i>Megabruchidius dorsalis</i>	1.000	[10] [*]
<i>Megabruchidius tonkineus</i>	0.977	[10] [*]
<i>Meleagris gallopavo</i>	0.450	[40]
<i>Molothrus ater</i>	0.455	[41]
<i>Myodes glareolus</i>	0.353	[42]
<i>Nerodia sipedon</i>	0.556	[43]
<i>Notiomystis cincta</i>	0.836	[44]
<i>Oncorhynchus clarkii</i>	0.552	[45]
<i>Onthophagus taurus</i>	0.789	[46]
<i>Paracerceis sculpta</i>	0.667	[47]
<i>Physa acuta</i>	0.789	[48]
<i>Poecilia gillii</i>	0.709	[49]
<i>Poecilia reticulata</i>	0.710	[50]
<i>Pycnogonum stearnsi</i>	0.686	[51]
<i>Radix balthica</i>	0.500	[52]
<i>Salmo trutta</i>	0.680	[53]
<i>Schmidtea polychroa</i>	0.918	[54]
<i>Sialia currucoides</i>	0.342	[55]
<i>Spermophilus columbianus</i>	0.343	[56]
<i>Strongylocentrotus franciscanus</i>	0.990	[57]
<i>Strongylocentrotus purpuratus</i>	0.990	[57]
<i>Syngnathus floridae</i>	0.633	[58]
<i>Syngnathus scovelli</i>	0.615	[59]
<i>Syngnathus typhle</i>	0.528	[60]
<i>Tamias amoenus</i>	0.595	[61]
<i>Tamias striatus</i>	0.650	[62]
<i>Taricha granulosa</i>	0.548	[63]
<i>Tribolium castaneum</i>	0.661	**
<i>Xerospermophilus tereticaudus</i>	0.935	[64]
<i>Xiphophorus birchmanni</i>	0.839	[32]
<i>Xiphophorus helleri</i>	0.638	[65]
<i>Zonotrichia albicollis</i>	0.306	[66]
<i>Zonotrichia leucophrys</i>	0.346	[67]
<i>Zootoca vivipara</i>	0.633	[68]

* Unpublished study by Fromontiel and colleagues.

** Unpublished study by Winkler and colleagues.

[†] Authors of primary studies provided on request additional data to compute polyandry.

[¶] References could only be found for classification of the mating system. Polyandry was extrapolated from the average level of polyandry observed in low-polyandry and high-polyandry species, respectively.

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Table E. Global tests of sexual selection in females excluding data on sex-role reversed species. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the dataset excluding sex-role reversed species (global model) and subsets with respect to mating success method (copulatory *versus* genetic), mating success range (including *versus* excluding zero mating success category), study type (laboratory *versus* field studies) and mating system (low-polyandry *versus* high-polyandry species). Table shows number of effect sizes (k), number of species (N), effect size (r), and heterogeneity I^2 arising from phylogenetic affinities, between-study variation, and between-observation variation. Model estimates are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Model	k	N_{Species}	Effect size		Heterogeneity				
			r		P_{MCMC}	$I^2_{\text{Phylogeny}}$	I^2_{Study}	$I^2_{\text{Observation}}$	
Global model (non-phylogenetic)	109	71	0.38	(0.31, 0.45)	< 0.001	-	-	-	-
Global model (phylogenetic)	109	71	0.35	(0.20, 0.49)	0.002	0.15	(0.00, 0.49)	0.66	(0.33, 0.91)
Copulatory mating success	41	22	0.22	(0.08, 0.37)	0.008	0.30	(0.01, 0.72)	0.22	(0.00, 0.59)
Genetic mating success	70	52	0.46	(0.29, 0.64)	0.001	0.16	(0.00, 0.51)	0.66	(0.28, 0.94)
Including zero mating success	59	36	0.41	(0.22, 0.57)	0.002	0.20	(0.00, 0.63)	0.54	(0.08, 0.90)
Excluding zero mating success	77	56	0.31	(0.12, 0.50)	0.007	0.24	(0.00, 0.67)	0.62	(0.21, 0.94)
Laboratory studies	43	27	0.38	(0.18, 0.56)	0.002	0.27	(0.00, 0.74)	0.37	(0.00, 0.78)
Field studies	66	45	0.31	(0.00, 0.56)	0.062	0.28	(0.00, 0.79)	0.58	(0.10, 0.93)
Low-polyandry species	32	16	0.22	(-0.02, 0.45)	0.066	0.24	(0.00, 0.68)	0.53	(0.01, 0.90)
High-polyandry species	77	55	0.38	(0.17, 0.58)	0.003	0.45	(0.07, 0.81)	0.28	(0.00, 0.64)
									0.14 (0.00, 0.37)

Table F. Predictors of inter-specific variation in female Bateman gradients excluding data on sex-role reversed species. Methodological moderators include mating success method (copulatory *versus* genetic mating success), mating success range (including *versus* excluding zero mating success category), study type (field *versus* lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Model estimates (i.e., estimated difference between groups) are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals obtained from phylogenetically controlled General Linear-Mixed Effects Models. The variance explained by the moderator variable is given as the marginal R^2 with 95% HPD intervals in parentheses.

Moderator	Estimate		P_{MCMC}	R^2	
Mating success method	0.31	(0.17, 0.46)	< 0.001	0.22	(0.16, 0.29)
Mating success range	0.09	(0.02, 0.17)	0.016	0.02	(0.01, 0.03)
Study type	0.04	(-0.14, 0.23)	0.675	0.00	(0.00, 0.01)
Year of publication	0.00	(-0.01, 0.01)	0.729	0.00	(0.00, 0.00)
Mating system	0.28	(0.12, 0.43)	0.001	0.16	(0.10, 0.22)
Polyandry	0.62	(0.32, 0.91)	< 0.001	0.23	(0.14, 0.32)

Table G. Global tests of sexual selection in females excluding data on humans. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the dataset including all species except humans (global model) and subsets with respect to mating success method (copulatory *versus* genetic), mating success range (including *versus* excluding zero mating success category), study type (laboratory *versus* field studies) and mating system (low-polyandry *versus* high-polyandry species). Table shows number of effect sizes (k), number of species (N), effect size (r), and heterogeneity I^2 arising from phylogenetic affinities, between-study variation, and between-observation variation. Model estimates are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Model	k	N_{Species}	Effect size		Heterogeneity				
			r		P_{MCMC}	$I^2_{\text{Phylogeny}}$	I^2_{Study}	$I^2_{\text{Observation}}$	
Global model (non-phylogenetic)	110	76	0.44	(0.37, 0.51)	< 0.001	-	-	-	-
Global model (phylogenetic)	110	76	0.39	(0.19, 0.58)	0.002	0.25	(0.00, 0.69)	0.49	(0.03, 0.74)
Copulatory mating success	33	23	0.28	(0.11, 0.44)	0.009	0.02	(0.00, 0.66)	0.02	(0.00, 0.44)
Genetic mating success	79	56	0.50	(0.29, 0.70)	0.001	0.01	(0.00, 0.67)	0.68	(0.16, 0.91)
Including zero mating success	64	41	0.47	(0.26, 0.66)	< 0.001	0.01	(0.00, 0.74)	0.02	(0.00, 0.71)
Excluding zero mating success	74	57	0.33	(0.10, 0.56)	0.012	0.47	(0.01, 0.79)	0.35	(0.00, 0.78)
Laboratory studies	52	31	0.41	(0.13, 0.65)	0.007	0.72	(0.11, 0.92)	0.01	(0.00, 0.51)
Field studies	58	46	0.41	(0.18, 0.61)	0.007	0.01	(0.00, 0.63)	0.71	(0.04, 0.89)
Low-polyandry species	22	15	0.25	(0.00, 0.48)	0.056	0.02	(0.00, 0.56)	0.01	(0.00, 0.83)
High-polyandry species	88	61	0.41	(0.15, 0.67)	0.005	0.75	(0.27, 0.92)	0.01	(0.00, 0.41)
									0.01 (0.00, 0.31)

Table H. Predictors of inter-specific variation in female Bateman gradients excluding data on humans. Methodological moderators include mating success method (copulatory *versus* genetic mating success), mating success range (including *versus* excluding zero mating success category), study type (field *versus* lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Model estimates (i.e., estimated difference between groups) are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals obtained from phylogenetically controlled General Linear-Mixed Effects Models. The variance explained by the moderator variable is given as the marginal R^2 with 95% HPD intervals in parentheses.

Moderator	Estimate	P_{MCMC}	R^2
Mating success method	0.28 (0.09, 0.46)	0.003	0.16 (0.10, 0.21)
Mating success range	0.12 (0.04, 0.20)	0.002	0.03 (0.02, 0.05)
Study type	0.05 (-0.13, 0.22)	0.563	0.01 (0.00, 0.01)
Year of publication	0.00 (-0.02, 0.01)	0.528	0.00 (0.00, 0.01)
Mating system	0.27 (0.10, 0.43)	0.002	0.10 (0.05, 0.14)
Polyandry	0.60 (0.25, 0.94)	0.001	0.09 (0.05, 0.15)

Supplementary Information – S1 Text

Sexual selection in females and the evolution of polyandry

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This Supplementary Information file includes:

Figures A - E

Tables A - H

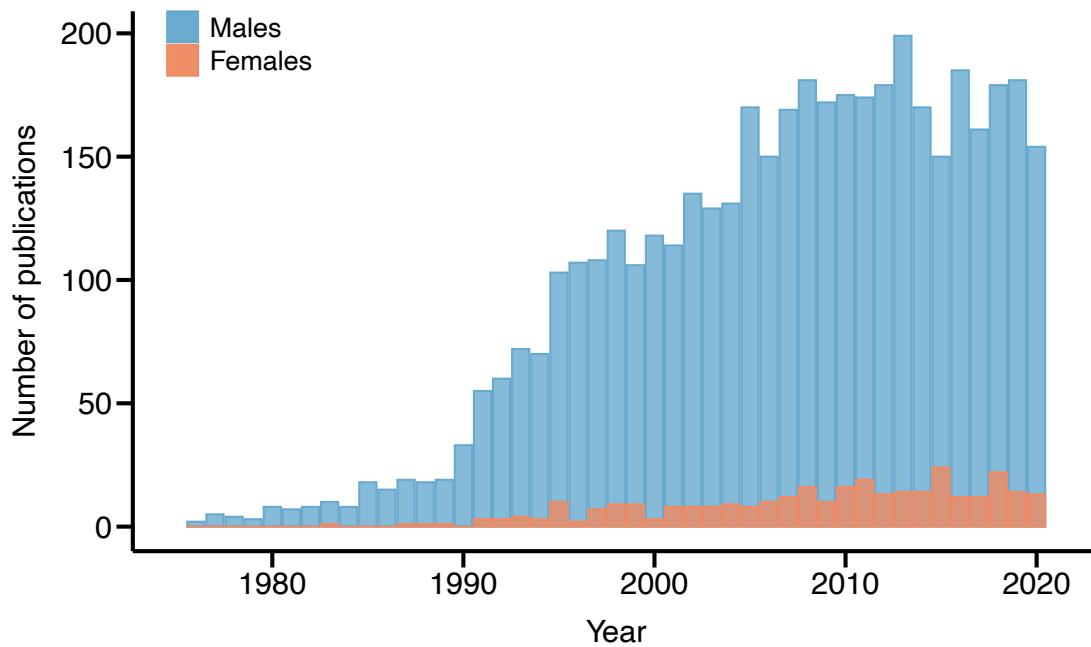


Figure A. Imbalance between studies of sexual selection in males and females. Bars indicate a strong male bias in the number of published articles on sexual selection indexed in ISI Web of Science (Clarivate Analytics) between 1900-2021. Data obtained from topic search using the search terms “sexual selection AND (male choice OR female competition)” for female and “sexual selection AND female choice OR male competition” for male search. This is not meant to provide an exhaustive search of publications on sexual selection but to showcase the publication bias towards male studies focusing on Darwinian sexual selection in terms of competition for and choice of mating partners.

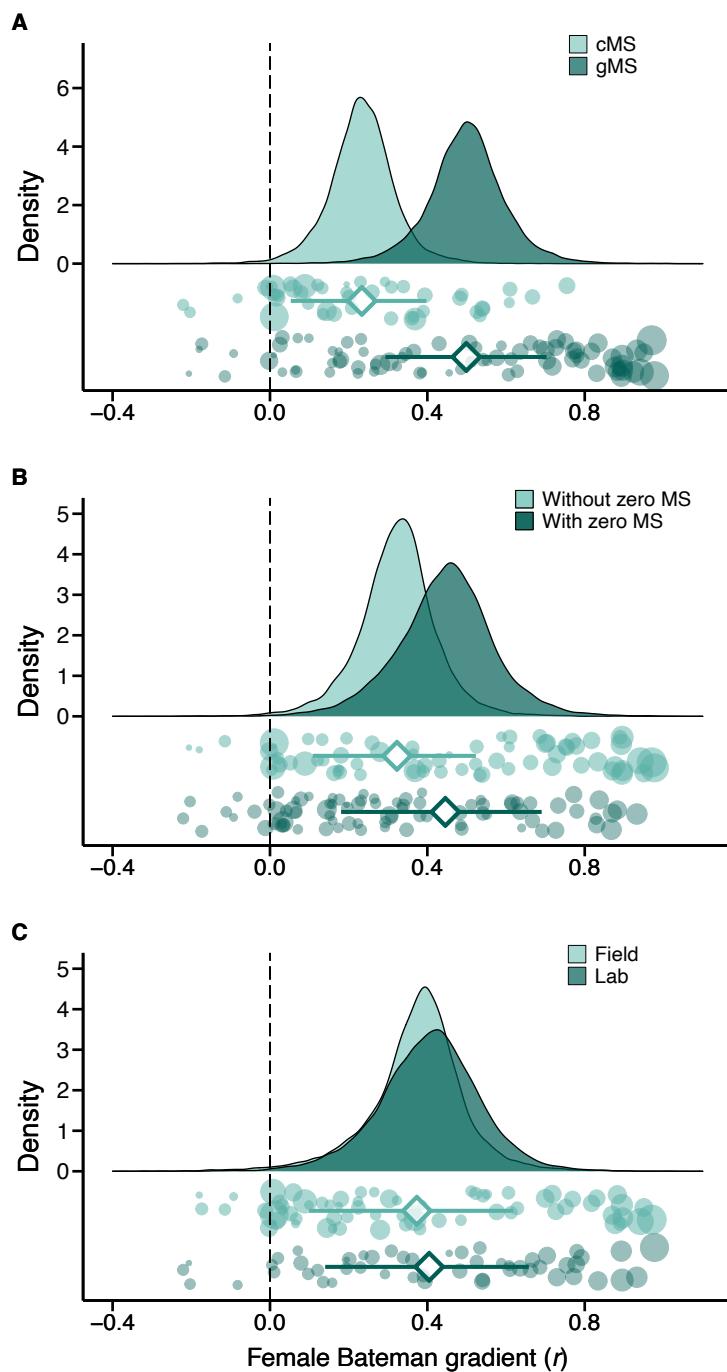


Figure B. Methodological predictors of female Bateman gradients. Raincloud charts showing effects of mating success method (*cMS*: copulatory mating success, *gMS*: genetic mating success), mating success range (with or without zero mating success (MS) category) and study type (field versus laboratory studies) on female Bateman gradients (see also Table 2 and Table C in S1 Text). The code and data needed to generate this figure can be found at https://salomefromonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

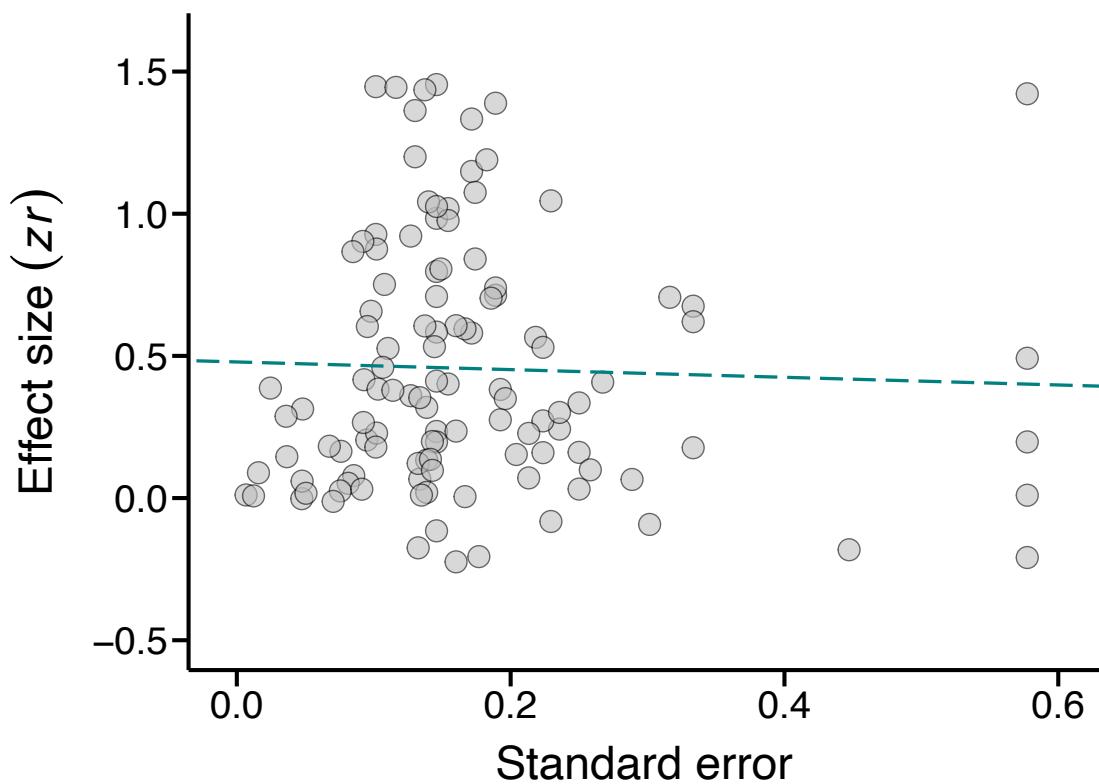


Figure C. Egger's regression. Relationship between effect size Fisher's z and its standard error testing whether small studies (i.e., those with smaller sample sizes and lower precision) are more likely to be published when reporting larger effect sizes. Dashed line shows the regression fit. The code and data needed to generate this figure can be found at https://salomefrommonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

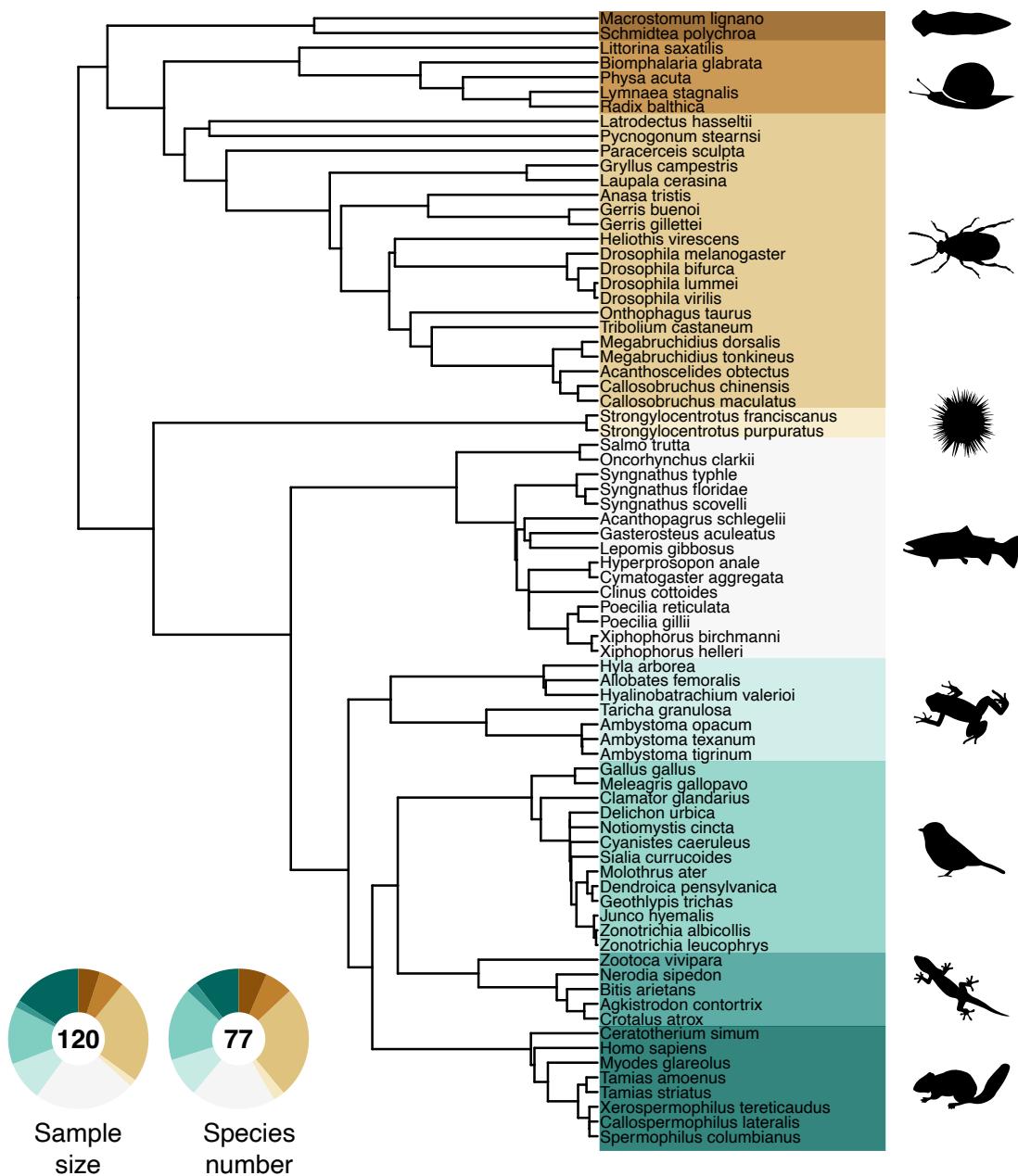


Figure D. Phylogenetic tree of all sampled species. Doughnut charts show the relative fraction of the sampled effect sizes (i.e., number of Bateman gradients) and the number of species.

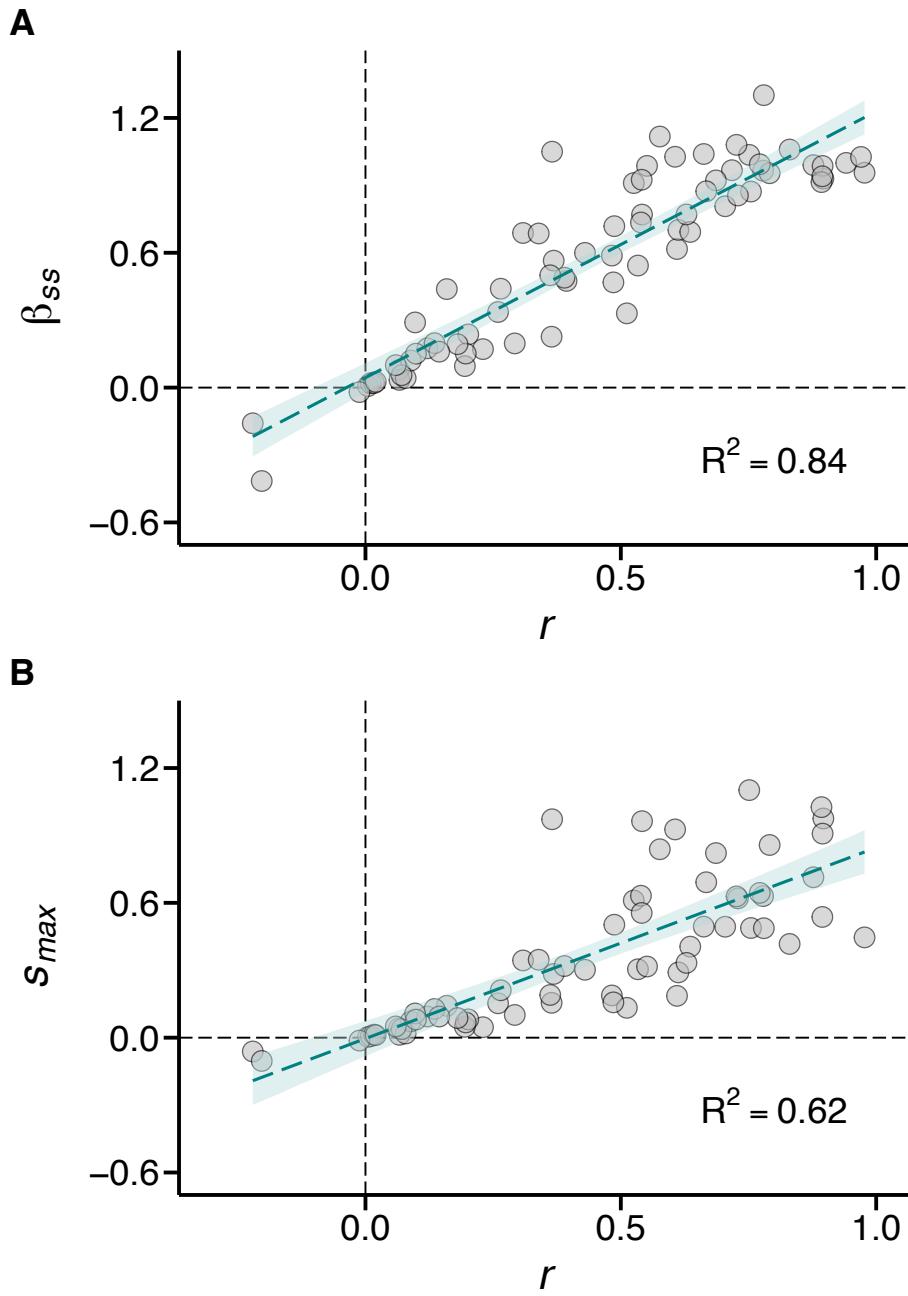


Figure E. Significance of used effect size. Relationship between effect size r (correlation coefficient) and (A) the actual Bateman gradient (β_{ss}) and (B) the maximum standardized sexual selection differential (s'_{max}). Graphs show a subset of data for which (A) standardized Bateman gradients were available ($N = 74$) and (B) estimates of the variance in relativized mating success could be extracted from primary studies ($N = 73$). Dashed line shows the linear regression fit with shaded area indicating the 95% confidence intervals. The code and data needed to generate this figure can be found at https://salomefrommonteil.github.io/META_SexSelFem/ and <https://doi.org/10.5281/zenodo.7303598>.

Table A. Global tests of sexual selection in females using the restricted maximum likelihood (REML) approach. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the entire dataset (global model) and subsets with respect to mating success method (copulatory versus genetic), mating success range (including versus excluding zero mating success category), study type (laboratory versus field studies) and mating system (low-polyandry versus high-polyandry species). Table shows number of effect sizes (k), number of species (N) and estimates of r together with 95% confidence intervals (in parentheses).

Model	k	N_{Species}	Global effect size			P -value
			r	(95% CI)	z -value	
Global model	120	77	0.37	(0.15, 0.59)	3.33	0.001
Copulatory mating success	43	24	0.23	(0.06, 0.41)	2.66	0.008
Genetic mating success	79	56	0.50	(0.32, 0.68)	5.41	< 0.001
Including zero mating success	70	42	0.43	(0.18, 0.68)	3.34	0.001
Excluding zero mating success	79	58	0.32	(0.17, 0.48)	4.09	< 0.001
Laboratory studies	52	31	0.40	(0.15, 0.65)	3.10	0.002
Field studies	68	47	0.40	(0.31, 0.49)	8.96	< 0.001
High-polyandry species	32	16	0.23	(0.09, 0.37)	3.16	0.002
Low-polyandry species	88	61	0.41	(0.16, 0.66)	3.20	0.001

Table B. Comparison of Bateman gradients among major taxonomic groups.

Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown all classes for which at least 10 effect sizes have been obtained from the literature. Table shows number of effect sizes (k), number of species (N), and effect sizes (r) with posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Taxonomic group	k	N_{Species}	Effect size		P_{MCMC}
			r	(Posterior mode, HPD)	
Arthropoda	29	20	0.38	(0.25, 0.52)	< 0.001
Actinopterygii	28	15	0.59	(0.45, 0.73)	< 0.001
Amphibia	11	7	0.47	(0.21, 0.72)	0.005
Aves	16	13	0.37	(0.20, 0.51)	< 0.001
Mammalia	19	8	0.37	(0.15, 0.60)	0.004

Table C. Predictors of inter-specific variation in female Bateman gradients using restricted maximum likelihood (REML) approach. Methodological moderators include mating success method (copulatory versus genetic mating success), mating success range (including versus excluding mating success category), study type (field versus lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry (continuous variable) estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Phylogenetically controlled multilevel meta-analytic single predictor models are shown with Omnibus tests (Wald-type chi-square test) and McFadden's R^2 .

Moderator	Estimate \pm SE	Q_M	P-value	R^2
Mating success method	0.28 \pm 0.09	10.71	0.001	0.23
Mating success range	0.16 \pm 0.06	6.48	0.011	0.14
Study type	0.07 \pm 0.09	0.62	0.429	0.03
Year	0.00 \pm 0.01	0.67	0.414	0.01
Mating system	0.31 \pm 0.07	16.92	< 0.001	0.35
Polyandry	0.66 \pm 0.14	23.30	< 0.001	0.47

Table D. Estimates of polyandry used to assess the mating system classification (low-polyandry and high-polyandry species). Table shows estimates of all 77 sampled species in alphabetical order together with reference.

Species	Polyandry	Reference
<i>Acanthopagrus schlegelii</i>	0.920	[1]
<i>Acanthoscelides obtectus</i>	0.551	*
<i>Agkistrodon contortrix</i>	0.520	[2]
<i>Allobates femoralis</i>	0.571	[3]
<i>Ambystoma opacum</i>	0.294	[4]
<i>Ambystoma texanum</i>	0.857	[5]
<i>Ambystoma tigrinum</i>	0.467	[6]
<i>Anasa tristis</i>	0.950	[7]
<i>Biomphalaria glabrata</i>	0.654	[8]
<i>Bitis arietans</i>	0.941	[9]
<i>Callosobruchus chinensis</i>	0.680	[10] †
<i>Callosobruchus maculatus</i>	1.000	[10] †
<i>Callospermophilus lateralis</i>	0.630	[11]
<i>Ceratotherium simum</i>	0.697	[12]
<i>Clamator glandarius</i>	0.308	[13]
<i>Clinus cottoides</i>	0.826	[14]
<i>Crotalus atrox</i>	0.400	[15]
<i>Cyanistes caeruleus</i>	0.470	[16]
<i>Cymatogaster aggregata</i>	0.800	[17]
<i>Delichon urbica</i>	0.235	[18]
<i>Dendroica pensylvanica</i>	0.606	[19]
<i>Drosophila bifurca</i>	0.326	[20] ††
<i>Drosophila lummei</i>	0.753	[21] ††
<i>Drosophila melanogaster</i>	0.759	[22]
<i>Drosophila virilis</i>	0.753	[21] ††
<i>Gallus gallus</i>	0.950	[23] †
<i>Gasterosteus aculeatus</i>	0.783	[24]
<i>Geothlypis trichas</i>	0.654	[25]
<i>Gerris buenoi</i>	1.000	[26]
<i>Gerris gillettei</i>	0.776	[27]
<i>Gryllus campestris</i>	0.809	[28]
<i>Heliothis virescens</i>	0.655	[29]
<i>Homo sapiens</i>	0.012	[30]
<i>Hyalinobatrachium valerioi</i>	0.736	[31]
<i>Hyla arborea</i>	0.158	[32]
<i>Hyperprosopon analis</i>	1.000	[17]
<i>Junco hyemalis</i>	0.439	[33]
<i>Latrodectus hasselti</i>	0.667	[34]
<i>Laupala cerasina</i>	1.000	[35]
<i>Lepomis gibbosus</i>	0.244	[36]

Species	Polyandry	Reference
<i>Littorina saxatilis</i>	0.680	[37]
<i>Lymnaea stagnalis</i>	0.588	[38]
<i>Macrostomum lignano</i>	1.000	[39]
<i>Megabruchidius dorsalis</i>	1.000	[10] [*]
<i>Megabruchidius tonkineus</i>	0.977	[10] [*]
<i>Meleagris gallopavo</i>	0.450	[40]
<i>Molothrus ater</i>	0.455	[41]
<i>Myodes glareolus</i>	0.353	[42]
<i>Nerodia sipedon</i>	0.556	[43]
<i>Notiomystis cincta</i>	0.836	[44]
<i>Oncorhynchus clarkii</i>	0.552	[45]
<i>Onthophagus taurus</i>	0.789	[46]
<i>Paracerceis sculpta</i>	0.667	[47]
<i>Physa acuta</i>	0.789	[48]
<i>Poecilia gillii</i>	0.709	[49]
<i>Poecilia reticulata</i>	0.710	[50]
<i>Pycnogonum stearnsi</i>	0.686	[51]
<i>Radix balthica</i>	0.500	[52]
<i>Salmo trutta</i>	0.680	[53]
<i>Schmidtea polychroa</i>	0.918	[54]
<i>Sialia currucoides</i>	0.342	[55]
<i>Spermophilus columbianus</i>	0.343	[56]
<i>Strongylocentrotus franciscanus</i>	0.990	[57]
<i>Strongylocentrotus purpuratus</i>	0.990	[57]
<i>Syngnathus floridae</i>	0.633	[58]
<i>Syngnathus scovelli</i>	0.615	[59]
<i>Syngnathus typhle</i>	0.528	[60]
<i>Tamias amoenus</i>	0.595	[61]
<i>Tamias striatus</i>	0.650	[62]
<i>Taricha granulosa</i>	0.548	[63]
<i>Tribolium castaneum</i>	0.661	**
<i>Xerospermophilus tereticaudus</i>	0.935	[64]
<i>Xiphophorus birchmanni</i>	0.839	[32]
<i>Xiphophorus helleri</i>	0.638	[65]
<i>Zonotrichia albicollis</i>	0.306	[66]
<i>Zonotrichia leucophrys</i>	0.346	[67]
<i>Zootoca vivipara</i>	0.633	[68]

* Unpublished study by Fromontiel and colleagues.

** Unpublished study by Winkler and colleagues.

[†] Authors of primary studies provided on request additional data to compute polyandry.

[¶] References could only be found for classification of the mating system. Polyandry was extrapolated from the average level of polyandry observed in low-polyandry and high-polyandry species, respectively.

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Table E. Global tests of sexual selection in females excluding data on sex-role reversed species. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the dataset excluding sex-role reversed species (global model) and subsets with respect to mating success method (copulatory *versus* genetic), mating success range (including *versus* excluding zero mating success category), study type (laboratory *versus* field studies) and mating system (low-polyandry *versus* high-polyandry species). Table shows number of effect sizes (k), number of species (N), effect size (r), and heterogeneity I^2 arising from phylogenetic affinities, between-study variation, and between-observation variation. Model estimates are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Model	k	N_{Species}	Effect size		Heterogeneity				
			r		P_{MCMC}	$I^2_{\text{Phylogeny}}$	I^2_{Study}	$I^2_{\text{Observation}}$	
Global model (non-phylogenetic)	109	71	0.38	(0.31, 0.45)	< 0.001	-	-	-	-
Global model (phylogenetic)	109	71	0.35	(0.20, 0.49)	0.002	0.15	(0.00, 0.49)	0.66	(0.33, 0.91)
Copulatory mating success	41	22	0.22	(0.08, 0.37)	0.008	0.30	(0.01, 0.72)	0.22	(0.00, 0.59)
Genetic mating success	70	52	0.46	(0.29, 0.64)	0.001	0.16	(0.00, 0.51)	0.66	(0.28, 0.94)
Including zero mating success	59	36	0.41	(0.22, 0.57)	0.002	0.20	(0.00, 0.63)	0.54	(0.08, 0.90)
Excluding zero mating success	77	56	0.31	(0.12, 0.50)	0.007	0.24	(0.00, 0.67)	0.62	(0.21, 0.94)
Laboratory studies	43	27	0.38	(0.18, 0.56)	0.002	0.27	(0.00, 0.74)	0.37	(0.00, 0.78)
Field studies	66	45	0.31	(0.00, 0.56)	0.062	0.28	(0.00, 0.79)	0.58	(0.10, 0.93)
Low-polyandry species	32	16	0.22	(-0.02, 0.45)	0.066	0.24	(0.00, 0.68)	0.53	(0.01, 0.90)
High-polyandry species	77	55	0.38	(0.17, 0.58)	0.003	0.45	(0.07, 0.81)	0.28	(0.00, 0.64)
									0.14 (0.00, 0.37)

Table F. Predictors of inter-specific variation in female Bateman gradients excluding data on sex-role reversed species. Methodological moderators include mating success method (copulatory *versus* genetic mating success), mating success range (including *versus* excluding zero mating success category), study type (field *versus* lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Model estimates (i.e., estimated difference between groups) are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals obtained from phylogenetically controlled General Linear-Mixed Effects Models. The variance explained by the moderator variable is given as the marginal R^2 with 95% HPD intervals in parentheses.

Moderator	Estimate		P_{MCMC}	R^2	
Mating success method	0.31	(0.17, 0.46)	< 0.001	0.22	(0.16, 0.29)
Mating success range	0.09	(0.02, 0.17)	0.016	0.02	(0.01, 0.03)
Study type	0.04	(-0.14, 0.23)	0.675	0.00	(0.00, 0.01)
Year of publication	0.00	(-0.01, 0.01)	0.729	0.00	(0.00, 0.00)
Mating system	0.28	(0.12, 0.43)	0.001	0.16	(0.10, 0.22)
Polyandry	0.62	(0.32, 0.91)	< 0.001	0.23	(0.14, 0.32)

Table G. Global tests of sexual selection in females excluding data on humans. Results of intercept-only phylogenetically controlled General Linear-Mixed Effects Models are shown for the dataset including all species except humans (global model) and subsets with respect to mating success method (copulatory *versus* genetic), mating success range (including *versus* excluding zero mating success category), study type (laboratory *versus* field studies) and mating system (low-polyandry *versus* high-polyandry species). Table shows number of effect sizes (k), number of species (N), effect size (r), and heterogeneity I^2 arising from phylogenetic affinities, between-study variation, and between-observation variation. Model estimates are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals in parentheses.

Model	k	N_{Species}	Effect size		Heterogeneity				
			r		P_{MCMC}	$I^2_{\text{Phylogeny}}$	I^2_{Study}	$I^2_{\text{Observation}}$	
Global model (non-phylogenetic)	110	76	0.44	(0.37, 0.51)	< 0.001	-	-	-	-
Global model (phylogenetic)	110	76	0.39	(0.19, 0.58)	0.002	0.25	(0.00, 0.69)	0.49	(0.03, 0.74)
Copulatory mating success	33	23	0.28	(0.11, 0.44)	0.009	0.02	(0.00, 0.66)	0.02	(0.00, 0.44)
Genetic mating success	79	56	0.50	(0.29, 0.70)	0.001	0.01	(0.00, 0.67)	0.68	(0.16, 0.91)
Including zero mating success	64	41	0.47	(0.26, 0.66)	< 0.001	0.01	(0.00, 0.74)	0.02	(0.00, 0.71)
Excluding zero mating success	74	57	0.33	(0.10, 0.56)	0.012	0.47	(0.01, 0.79)	0.35	(0.00, 0.78)
Laboratory studies	52	31	0.41	(0.13, 0.65)	0.007	0.72	(0.11, 0.92)	0.01	(0.00, 0.51)
Field studies	58	46	0.41	(0.18, 0.61)	0.007	0.01	(0.00, 0.63)	0.71	(0.04, 0.89)
Low-polyandry species	22	15	0.25	(0.00, 0.48)	0.056	0.02	(0.00, 0.56)	0.01	(0.00, 0.83)
High-polyandry species	88	61	0.41	(0.15, 0.67)	0.005	0.75	(0.27, 0.92)	0.01	(0.00, 0.41)
									0.01 (0.00, 0.31)

Table H. Predictors of inter-specific variation in female Bateman gradients excluding data on humans. Methodological moderators include mating success method (copulatory *versus* genetic mating success), mating success range (including *versus* excluding zero mating success category), study type (field *versus* lab) and year of publication (continuous variable). Effect of mating system contrasts low-polyandry and high-polyandry species. Effect of polyandry estimates the relationship between the female Bateman gradient and the proportion of polyandrous females in the population. Model estimates (i.e., estimated difference between groups) are shown as posterior modes with 95% Highest Posterior Density (HPD) intervals obtained from phylogenetically controlled General Linear-Mixed Effects Models. The variance explained by the moderator variable is given as the marginal R^2 with 95% HPD intervals in parentheses.

Moderator	Estimate	P_{MCMC}	R^2
Mating success method	0.28 (0.09, 0.46)	0.003	0.16 (0.10, 0.21)
Mating success range	0.12 (0.04, 0.20)	0.002	0.03 (0.02, 0.05)
Study type	0.05 (-0.13, 0.22)	0.563	0.01 (0.00, 0.01)
Year of publication	0.00 (-0.02, 0.01)	0.528	0.00 (0.00, 0.01)
Mating system	0.27 (0.10, 0.43)	0.002	0.10 (0.05, 0.14)
Polyandry	0.60 (0.25, 0.94)	0.001	0.09 (0.05, 0.15)